

09267006 092901
T06250 90025350

Figure 1

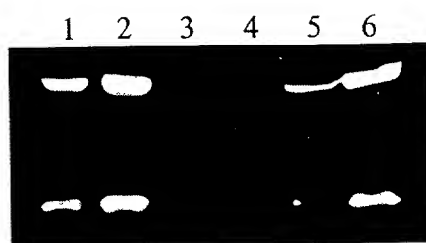


Figure 2

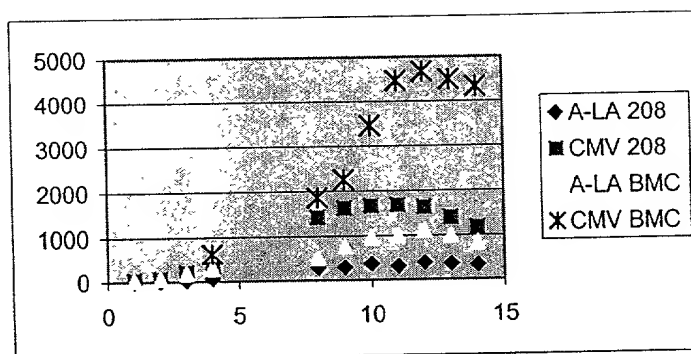


Figure 3

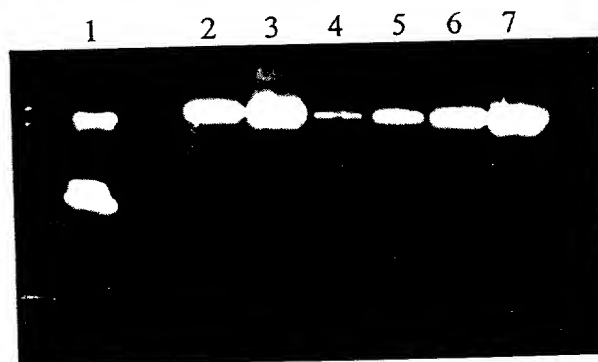


Figure 4
SEQ ID NO:1

Hybrid Human-Bovine Alpha-Lactalbumin Promoter

1 GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51 AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101 ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCACCTCGATGGACATGAGTTTGAGCAAGCTTCC
201 AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351 AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTGAGAA
651 CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTGATCCCTGG
751 CTTGGGAAGATCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGT
900 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCATGCAAGGGTCTCCTGC
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001 CTGGAGTGGGTAGCCTATTCTTCTCCAGGGGATCTTCCATCCCAGGAA
1051 TTGAACCTGGAGTCTCCTGCATTTTCAGGTGGATTCTTCACCAGCTGAAC
1101 CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTTTCAAGTTCTCCATTTTGTGAAATAGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751 CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801 GCAGGATCATGGTTTGAACCTTTTCTGGCCAGAGAACAATACCTGCTATG
1851 GACTAGATACTGGGAGAGGGAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951 CTCTTCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001 GAATATAAATATATGAACTGAGTGATGCTTCCATTTTCAGGTTCTTGGGG
2051 GCGCCGAATTTCGAGCTCGGTACCCGGGGATCTCGAGGGGGGGCCCGGTAC
2101 C

- 1 - 1525 Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
1526 - 2056 Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
2057 - 2101 Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

```
1      GATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCT
51     ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCG
101    GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151    GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201    AGGGTGAGATATCGGCCGGGGACGCGCGGTGGTAATTACAAGCG
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1 - 119      Mutated PPE
120 -126     Linker
127 - 245    Mutated PPE
```

09697006-062904

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

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1   GGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51  CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTCCACCATAT
101 TGCCGTCTTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTCTTG
151 ACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCT
201 GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251 CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGAC
301 AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAACCTGCAAAGGC
351 GGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401 AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451 GTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501 ATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGG
551 ACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTC
601 TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651 GATATCTAGATCTCGAGCTCGCGAAAGCTT

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1 - 583	IRES
584 - 640	Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680	Multiple cloning site

T05290-902650

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

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1   CGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAA
51  TATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACA
101 TTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTG
151 ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATA
201 TATGGAGTTCGCGCTTACATAACTTACGGTAAATGGCCCGCTGGCTGAC
251 CGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAT
301 GTAACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACG
351 GTAAACTGCCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGC
401 CCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAG
451 TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGT
501 CATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTG
551 GATAGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATGACGTC
601 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCAAAATGTCTG
651 TAACAACCTCCGCCCCATTGACGCCAAATGGGCGGTAGGCATGTACGGTGGG
701 AGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
751 CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
801 CCTCCGCGGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCA
851 CCATGGGATGGAGCTGTATCATCTCTTCTTGGTAGCAACAGCTACAGGT
901 GTCCACTCCGAGGTCCAACCTGGTGAGAGCGGTGGAGGTGTTGTGCAACC
951 TGGCCGGTCCCTGCGCCTGTCTGCTCCGCATCTGGCTTCGATTTACCA
1001 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
1051 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
1101 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
1151 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
1201 AGCCTTTACTTCGGCTTCCCCTGGTTGCTTATTGGGGCCAAGGGACCCC
1251 GGTCAACGCTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCTGG
1301 CACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
1351 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGC
1401 CCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTACAGTCTCAGGAC
1451 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
1501 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
1551 CAAGAGAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACATGCCACCGT
1601 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCA
1651 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGT
1701 GGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACG
1751 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
1801 TACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCTGCACCAGGA
1851 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCC
1901 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
1951 CCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCA
2001 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCG
2051 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
2101 CCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCT
2151 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
2201 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
2251 GGGAAATGAAAGCCGAATTCGCCCCCTCTCCCTCCCCCCCCCTAACGTTA
2301 CTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
2351 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGG
2401 CCTGTCTTCTTGACGAGCATTCTTAGGGGTCTTCCCCTCTCGCCAAAG
2451 GAATGCAAGGTCTGTTGAATGTCTGTGAAGGAAGCAGTTCTCTGGAAGCT
2501 TCTTGAAGACAAACAACGTCTGTAGCGACCCCTTGCAGGCAGCGGAACCC
2551 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
2601 CACCTGCAAAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTT
2651 GTGGAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAA
2701 GGATGCCCAAGAGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGT
2751 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCC
2801 CCGAACACGCGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGG

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T.06290 "062901

Figure 7b

2851 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
 2901 GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
 2951 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
 3001 TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
 3051 TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTAGCGGTAGCGG
 3101 TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
 3151 TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCTGTTCCGCCAA
 3201 GGGACCAAGGTGGAAATCAAACGAACCTGTGGCTGCACCATCTGTCTTCAT
 3251 CTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGT
 3301 GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
 3351 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGA
 3401 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAG
 3451 CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
 3501 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
 3551 TAGGCCTCCTAGGTGACATCGATAAAAATAAAAGATTTTATTTAGTCTCC
 3601 AGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCT
 3651 TAAGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGAGAATAGA
 3701 GAAGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGGCCAA
 3751 ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
 3801 GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGTAAGCAGTTC
 3851 CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
 3901 CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
 3951 CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCG
 4001 CTTCTGTTGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCAAC
 4051 CCTCACTCGGGGCGCCAGTCTCCGATTGACTGAGTCGCCCCGGGTACCC
 4101 GTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTG
 4151 TTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTAGCGGGGGTC
 4201 TTTCATT

- 1 - 812 CMV promoter/enhancer
- 853-855 MN14 antibody heavy chain gene signal peptide start codon
- 2257 - 2259 MN14 antibody heavy chain gene start codon
- 2271 - 2846 EMCV IRES
- 2847 - 2849 Bovine alpha-lactalbumin signal peptide start codon
- 2904 - 2906 First codon mature MN14 antibody light chain gene
- 3543 - 3544 MN14 antibody light chain gene stop codon
- 3614 - 4207 MoMuLV 3' LTR

Figure 8a
SEQ ID NO:5
CMV LL2 Vector

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1      GGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAAT
51     ATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACAT
101    TTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGA
151    CTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATAT
201    ATGGAGTTCGCGGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
251    GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG
301    TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGG
351    TAAACTGCCCCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
401    CCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGT
451    ACATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTC
501    ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGG
551    ATAGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATTGACGTCA
601    ATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT
651    AACAACTCCGCCCCATTGACGCCAAATGGGCGGTAGGCATGTACGGTGGGA
701    GGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGAC
751    GCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGC
801    CTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTTCAGGACCTCAC
851    CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
901    TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCT
951    GGGTCATCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACCTTTACTAG
1001   CTACTGGCTGCACTGGGTGAGGCACCTGGACAGGGTCTGGAATGGA
1051   TTGGATACATTAATCCTAGGAATGATTATACTGAGTACAATCAGAACTTC
1101   AAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACAT
1151   GGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTGTGCAA
1201   GAAGGGATATTACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTC
1251   TCCTCAGCCTCCACCAAGGGCCCCATCGGTCTTCCCCCTGGCACCCCTCCTC
1301   CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
1351   ACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCAGC
1401   GCGGTGCACACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCT
1451   CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA
1501   TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
1551   GAGCCCAAATCTTGTGACAAAATCAGCATGCCCACCGTGCCAGCACC
1601   TGAATCCTGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAGG
1651   ACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGAC
1701   GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
1751   GGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCA
1801   CGTACCGTGTGGTCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAAT
1851   GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCAT
1901   GCAGAAAACCATCTCCAAGGCCAAGGGCAGCCCCGAGAACCACAGGTGT
1951   ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTG
2001   ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA
2051   GAGCAATGGGCAGCCGGAGAACAATAAGACCACGCCTCCCGTGTCTGG
2101   ACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGC
2151   AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCT
2201   GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAATGAA
2251   AGCCGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAG
2301   CCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCA
2351   TATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTC
2401   TTGACGAGCATTCCTAGGGGTCTTCCCCCTCTCGCCAAAGGAATGCAAGG
2451   TCTGTTGAATGTGCTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGAC
2501   AAACAACGTCTGTAGCGACCCCTTTCAGGCGAGCGGAACCCCCACCTGGC
2551   GACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA
2601   GCGGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
2651   TCAAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAG
2701   AAGGTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGTGCACATGCTT
2751   TACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCCGGAACCAG
2801   GGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTCCTTTGT

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T06290-00046860

Figure 8b

2851 CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
 2901 AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGGAGATAGGGTC
 2951 ACTATGAGCTGTAAGTCCAGTCAAAGTGTTTATACAGTGCAAATCACAA
 3001 GAACTACTTGGCCTGGTACCAGCAGAAACCAGGGAAAGCACCTAAACTGC
 3051 TGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTTCGCGATTCTCT
 3101 GGCAGCGGATCTGGGACAGATTTTACTTTCACCATCAGCTCTCTTCAACC
 3151 AGAAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT
 3201 TCGGTGGAGGGACCAAGGTGCAGATCAAACGAACTGTGGCTGCACCATCT
 3251 GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTC
 3301 TGTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
 3351 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCA
 3401 GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCT
 3451 GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
 3501 ATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT
 3551 TAGAGATCTAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATT
 3601 TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCA
 3651 AGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTG
 3701 AGAATAGAGAAGTTTCAAGGTCAAGGTGAGAACAGATGGAACAGCTGAATA
 3751 TGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCGGCTCAGGGC
 3801 CAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
 3851 AGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCAGATGCG
 3901 GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCC
 3951 CCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
 4001 GCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
 4051 CCCACAACCCCTCACTCGGGGCGCCAGTCTCCGATTGACTGAGTCGCCC
 4101 GGGTACCCGTGTATCCAATAAACCCCTCTGCAGTTGCATCCGACTTGTGG
 4151 TCTCGCTGTTCCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG
 4201 GTCTTTCATT

1 - 812 CMV promoter/enhancer
 852 - 854 LL2 antibody heavy chain signal peptide start codon
 2247 - 2249 LL2 antibody heavy chain stop codon
 2261 - 2836 EMCV IRES
 2837 - 2839 Bovine alpha-lactalbumin signal peptide start codon
 2894-2896 First codon of mature LL2 antibody light chain gene
 3551 - 3553 LL2 antibody light chain gene stop codon
 3622 - 4210 MoMuLV 3' LTR

095700-9004550

Figure 9a
SEQ ID NO:6
MMTV MN14 Vector

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1      CGAGCTTGGCAGAAATGGTTGAACTCCCGAGAGTGTCTACACCTAGGGG
51     AGAAGCAGCCAAGGGGTGTTTTCCACCAAGGACGACCCGTCTGCGCACA
101    AACGGATGAGCCCATCAGACAAAGACATATTCATTCTCTGCTGCAAACCTT
151    GGCATAGCTCTGCTTTGCCTGGGGCTATTGGGGGAAGTTGCGGTTTCGTGC
201    TCGCAGGGCTCTCACCCTTGACTCTTTCAATAATAACTCTTCTGTGCAAG
251    ATTACAATCTAAACAATTTCGAGAACTCGACCTTCCTCCTGAGGCAAGGA
301    CCACAGCCAACCTTCCTCTTACAAGCCGCATCGATTTTGTCTTCAGAAAT
351    AGAAATAAGAATGCTTGCTAAAAATTATATTTTACCAATAAGACCAATC
401    CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTATCTTTT
451    AGTACTATTTTTACTCAAATTCAGAAGTTAGAAATGGGAATAGAAAATAG
501    AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
551    CAGGCCTAGAAGTAAAAAAGGGAAAAAGAGTGTTTTTGTCAAATAGGA
601    GACAGGTGGTGGCAACCAGGGACTTATAGGGGACCTTACATCTACAGACC
651    AACAGATGCCCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
701    GGTGGGTTACAGTCAATGGCTATAAAGTGTTATATAGATCCCTCCCCTTT
751    CGTGAAAGACTCGCCAGAGCTAGACCTCCTTGGTGTATGTTGTCTCAAGA
801    AAAGAAAGACGACATGAAACAACAGGTACATGATTATATTTATCTAGGAA
851    CAGGAATGCACTTTTGGGGAAAGATTTTCCATACCAAGGAGGGGACAGTG
901    GCTGGACTAATAGAACATTATTTCTGCAAAAACCTTATGGCATGAGTTATTA
951    TGATTAGCCTTGATTTGCCCAACCTTGCGGTTCCCAAGGCTTAAGTAAGT
1001   TTTTGGTTACAAACTGTTCTTAAAAACAAGGATGTGAGACAAGTGGTTTCC
1051   TGACTTGGTTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTTCTATT
1101   TTCCTATGTTCTTTTGGAAATTTATCCAAATCTTATGTAAATGCTTATGTA
1151   AACCAAGATATAAAGAGTGCTGATTTTTTGTAGTAAACTTGCAACAGTCC
1201   TAACATTACCTCTTGTGTGTTTGTGTCTGTTCCGCATCCCGTCTCCGCT
1251   CGTCACTTATCCTTCACTTTCCAGAGGGTCCCCCGCAGACCCCGCGAC
1301   CCTCAGGTACGCCGCACTGCGGCAGCTGGCGCGCGAACAGGGACCCTCGGA
1351   TAAGTGACCCTTGTCTTTATTTCTACTATTTTGTGTTCTGTTTGT
1401   CTCTATCTTGTCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
1451   GAACCAAGCTAGCCCCGGGGTCGACGGATCCGATTACTTACTGGCAGGTGC
1501   TGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTC
1551   GACCAGGGTGAGATATCGGCCGGGGACGCGCGGGTGGTAATTACAAGCGA
1601   GATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAA
1651   CATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGG
1701   ACGCGCGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTACAGACCTCAC
1751   CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
1801   TCCACTCCGAGGTCCAACCTGGTGGAGAGCGGTGGAGGTGTTGTGCAACCT
1851   GGCCGGTCCCTGCGCCTGCTCCTGCTCCGCATCTGGCTTCGATTTACACCAC
1901   ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGA
1951   TTGGAGAAATTCATCCAGATAGCAGTACGATTAAGTATGCGCCGTCTCTA
2001   AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCCT
2051   GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTGTGCAA
2101   GCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCCG
2151   GTCACCGTCTCCTCAGCCTCCACCAAGGGGCCATCGGTCTTCCCCCTGGC
2201   ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
2251   TCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGGAACCTCAGGCGCC
2301   CTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACT
2351   CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
2401   AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
2451   AAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCACCGTG
2501   CCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAA
2551   AACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
2601   GTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGT
2651   GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
2701   ACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACAGGAC
2751   TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
2801   AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC

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T06290-90026850

Figure 9b

2851 CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
 2901 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
 2951 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
 3001 CCGTGCTGGAATCCGACGGCTCCTTCTTCCCTCTATAGCAAGCTCACCGTG
 3051 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
 3101 CGAGGCTCTGCACAACCCTACACGCAGAAAGAGCCTCTCCCTGTCTCCCG
 3151 GGAAATGAAAGCCGAATTCGCCCCCTCTCCCTCCCCCCCCCTAACGTTAC
 3201 TGGCCGAAGCCGCTTGGAAATAAGGCCGGTGTGCGTTTGTCTATATGTTAT
 3251 TTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGC
 3301 CCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGG
 3351 AATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCTT
 3401 CTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCC
 3451 CCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
 3501 ACCTGCAAAGGGCGGCACAACCCCAAGTCCACGTTGTGAGTTGGATAGTTG
 3551 TGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAG
 3601 GATGCCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTG
 3651 CACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCC
 3701 CGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGC
 3751 CTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCATGCCACCCAGG
 3801 CCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGT
 3851 GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGT
 3901 AGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACT
 3951 GGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTACGCGGTAGCGGT
 4001 AGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACAT
 4051 CGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTGCTTCGGCCAAG
 4101 GGACCAAGGTGGAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC
 4151 TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTG
 4201 CCTGCTGAATAAATTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGG
 4251 ATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGAC
 4301 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
 4351 AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 4401 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATCC
 4451 CCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGGA
 4501 TTACAAAATTTTGTGAAAGATTGACTGGTATTCTTAACATGTTGCTCCTT
 4551 TTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCT
 4601 TCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTC
 4651 TCTTTATGAGGAGTTGTGGCCCCGTGTGTCAGGCAACGTGGCGTGGTGTGCA
 4701 CTGTGTTTGTGTCAGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGT
 4751 CAGTCTCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGA
 4801 ACTCATCGCCGCTGCTTGCCTTCCCCGCTGCTGGACAGGGGCTCGGCTGTTGG
 4851 GCACTGACAAATCCGTGGTGTGTCGGGGAAATCATCGTCTTTTCTTGG
 4901 CTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTA
 4951 CGTCCCTTTCGGCCCTCAATCCAGCGGACCTTCTTCCCGCGGCCTGCTGC
 5001 CGGCTCTGCGGCCTCTTCCGCGTCTTCCGCTTCCGCTCAGACGAGTCGG
 5051 ATCTCCCTTTGGGCCGCTTCCCGCCTGATCGATAACCGTCAACATCGATA
 5101 AAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCC
 5151 CACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCAT
 5201 GGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTGAGGAACA
 5251 GATGGAACAGCTGAATATGGGCCAAAACAGGATATCTGTGGTAAGCAGTTC
 5301 CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
 5351 ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
 5401 GATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
 5451 GATGTTTCCAGGGTCCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTG
 5501 AACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCC
 5551 CGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTCTCTCC
 5601 GATTGACTGAGTCGCCCCGGTACCCGTGTATCCAATAAACCCCTCTTGCAG
 5651 TTGCATCCGACTTGTGGTCTCGCTGTTTCTTGGGAGGGTCTCCTCTGAGT
 5701 GATTGACTACCCGTCAGCGGGGTCTTTTCATT

1 - 1457 Mouse mammary tumor virus LTR
 1475 - 1726 Double mutated PPE sequence

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

1092906-062904

Figure 10a
SEQ ID NO:7
Alpha-Lactalbumin MN14 Vector

1 AAAGACCCACCCGCTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA
51 AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTTCAAGGTCA
101 GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTT
151 CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
201 AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAGAA
251 CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCAT
301 CAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
351 TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCGCT
401 CTCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTCT
451 TCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAATAAAGCCTCTTG
501 CTGTTTGCATCCGAATCGTGGTCTCGCTGTTTCCTTGGGAGGGTCTCCTCT
551 GAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCCGG
601 GATTTGGAGACCCCTGCCAGGGACCCAGCCACCACCGGGAGGTAAG
651 CTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTG
701 ATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAAGCTCTGTATCTGG
751 CGGACCCGTGGTGGAAGTACGAGTTCGAAACACCCGGCCGCAACCCTGG
801 GAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCGACCTGAGGAA
851 GGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGA
901 GACGAGAACCTAAAACAGTTCGCCCTCCGTCTGAATTTTGTCTTTCGGT
951 TTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
1001 TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGC
1051 CAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAGATGT
1101 CGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151 TTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGA
1201 GACGGCACCTTTAACCGAGACCTCATCACCCAGGTAAAGATCAAGGTCTT
1251 TTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCT
1301 GGGAAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACAC
1351 CCTAAGCCTCCGCCTCCTCTTCTCCATCCGCCCCGTCTCTCCCCCTTGA
1401 ACCTCCTCGTTGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTC
1451 CTTCTCTAGGCGCCGGAATTCGATCTGATCAAGAGACAGGATGAGGATC
1501 GTTTCGCATGATTGAACAAGATGGATTGCACGAGGTTCTCCGGCCGCTT
1551 GGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGGCTGC
1601 TCTGATGCCGCCGTGTTCCGGCTGTGACGCGAGGGGCGCCCGGTTCTTTT
1651 TGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAG
1701 CGCGGCTATCGTGGCTGGCCACGACGGCGGTTCCCTGCGCAGCTGTGCTC
1751 GACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGGCGAAGTGCC
1801 GGGCAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCA
1851 TCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
1901 CCATTGACACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCGGAT
1951 GGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGC
2001 TCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGC
2051 GAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGT
2101 GGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGG
2151 CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201 CTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGC
2251 TCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
2301 GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGC
2351 CATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTC
2401 GGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCT
2451 CATGCTGGAGTTCTTCCGCCACCCCGGGCTCGATCCCTCGCGAGTTGGT
2501 TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551 AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601 CCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2651 ATCCTAGAAGTACCGAAAATGCAAGAGCAAAGACGAAAACATGCCACACA
2701 TGAGGAATACCGATTCTCTCATTAACATATTACGCGCAGTTATCTGGGCT
2751 TAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCTCCA
2801 GAGGTTTCATTACTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCCTG

105290-9002550

Figure 10b

2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGGC
2901 CACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAA
2951 GATTGAAGGCAGGAGGAGAAGGATGACAGAGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCCAGGAGTTGGTA
3051 ATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGACTGAACTGAACTGATAGTGTAATCCATGGTACAGA
3151 ATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTTAGAATACCTTTAGTTTGGAAAGTCTTAAATTATTTACT
3251 TAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATATAACCAATATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATCCTAAACTCTAC
3451 ATGTTCCAGGACACTGATCTTAAAGCTCAGGTTTCAAGATCTTGTTTTATA
3501 GGCTCTAGGTGATATTGTGGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTTCGATCCCTGGCTTGGGAAGAT
3601 CCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGGATTGCAAAGAG
3701 TTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGTATACACCTGTG
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGCATTGCAGAAAG
3801 ATTCTTTACCATTCTGAGCCACCAGGGAAGCCCAAGAATACTGGAGTGGGT
3851 AGCCTATTCTCTTCCAGGGATCTTCCCATCCAGGAATTGAACCTGGAG
3901 TCTCCTGCATTTTCAAGGTGGATTCTTCAACAGCTGAACTACCAGGTGGATA
3951 CTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCACCTTTCCCAA
4001 AAGGTTGGGTCACTCTTTTTTAACTTCTGTGGCCTACTCTGAGGCTGTC
4051 TACAAGCTTATATATTTATGAACACATTTATTGCAAGTTGTTAGTTTATG
4101 ATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTGGTTGGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTATACACACTTT
4201 TCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGATCTAAGTTATAT
4251 GTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCCTGACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTCATGCCTGGGTTG
4351 AGTGGGCCATGACATATGTTCTGGGCCCTTGTACATGGCTGGATTGGTTG
4401 GACAAGTGCCAGCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGAAGCTCGGTAT
4501 AGAACCTTTATTGTATTTTCTGATTGCCCTCACTTCTTATATTGCCCCAT
4551 GCCCTTCTTTGTTCTCAAGTAACCAGAGACAGTGCTTCCAGAACCAAC
4601 CCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG
4651 GTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATTGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCACTTCTTCTCCTAGA
4801 TGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTCTGCATGAATATAAATA
4851 TATGAAACTGAGTGATGCTTCCATTTCAAGTTCTTGGGGGCGCCGAATTC
4901 GAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTTACTGGCAGGTG
4951 CTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCT
5001 CGACCAGGGTGAGATATCGGCCGGGACGCGGCGGTGGTAATTACAAGCG
5051 AGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG
5151 GACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCA
5201 CCATGGGATGGAGCTGTATCATCTCTTCTTGGTAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAAGTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
5301 TGGCCGGTCCCTCGCCTGTCTGCTCCGCATCTGGCTTCGATTTACCA
5351 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
5451 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTC
5501 TGCAAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTGTGCA
5551 AGCCTTTACTTTCGGCTTCCCTGCTTGGTTTATTTGGGGCCAAGGGACCC
5601 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCTCCTCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGC
5751 CCTGACCAAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACC
5851 CAGACCTACATCTGCAACGTGAATCACAAAGCCAGCAACACCAAGGTGGA
5901 CAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGT

0907005-062901

Figure 10c

5951 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCA
6001 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
6051 GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
6101 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
6151 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGA
6201 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
6251 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
6301 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
6351 GGTACGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
6401 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCT
6451 CCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGT
6501 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
6551 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
6601 GGGAAATGAAAGCCGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTA
6651 CTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
6701 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGG
6751 CCCTGTCTTCTTGACGAGCATTCTAGGGGTCTTCCCCTCTCGCCAAAG
6801 GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCT
6851 TCTTGAAGACAAACAACGTCTGTAGCGACCCCTTTCAGGCAGCGGAACCC
6901 CCACTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
6951 CACCTGCAAAAGCGCGCACAAACCCAGTGCCACGTTGTGAGTTGGATAGTT
7001 GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
7051 GGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGT
7101 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCC
7151 CCGAACACGCGGGACGTGGTTTCTCTTGA AAAACACGATGATAATATGG
7201 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
7251 GCCGACATCCAGCTGACCCAGAGCCCCAAGCAGCCTGAGCGCCAGCGTGGG
7301 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
7351 TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
7401 TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTACAGCGGTAGCGG
7451 TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501 TCGCCACCTAGCTACTGCCAGCAATATAGCCTCTATCGGTGCTTCGGCCAA
7551 GGGACCAAGGTGGAAATCAAACGAACCTGTGGCTGCACCATCTGTCTTCAT
7601 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGT
7651 GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
7701 GATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGA
7751 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAG
7801 CAGACTCAGGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCATCAGGGC
7851 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATC
7901 CCCCAGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGG
7951 ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCT
8001 TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGC
8051 TTCCCGTATGGCTTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGT
8101 CTCTTTATGAGGAGTTGTGGCCCGTTGTGAGGCAACGTGGCGTGGTGTGC
8151 ACTGTGTTTGTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
8201 TCAGCTCCTTTCCGGGACTTTTCGCTTTCCCTCCCTATTGCCACGGCGG
8251 AACTCATCGCCGCTGCTTGCCTGCCCCGCTGCTGGACAGGGGCTCGGCTGTTG
8301 GGCAGTGACAATTCGGTGGTGTGTCGGGGAAATCATCGTCTTTCTTG
8351 GCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCTTCTGCT
8401 ACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCTCTCCCGCGCCTGCTG
8451 CCGGCTCTGCGGCCTCTTCCGCGTCTTCGCTTTCGCTCAGACGAGTCG
8501 GATCTCCCTTTGGGCGCCTCCCGCCTGATCGATAACGTCAACATCGAT
8551 AAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACC
8601 CCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCA
8651 TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTGAGGAAC
8701 AGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT
8751 CCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCA
8801 AACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAAC
8851 AGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATC
8901 AGATGTTTCCAGGGTGCCCAAGGACCTGAAATGACCCTGTGCCTTATTT
8951 GAACTAACCAATCAGTTGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCC
9001 CCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTCCTC

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9051 CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCA
9101 GTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAG
9151 TGATTGACTACCCGTCAGCGGGGGTCTTTTCAAT

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	8.5	5	35
Occupation	1.2	0.8	0	2
Health status	0.7	0.4	0	1
Stress level	2.5	1.2	1	4
Life satisfaction	3.8	1.5	1	5
Resilience	4.2	1.8	1	6
Optimism	4.5	1.6	1	6
Gratitude	4.8	1.4	1	6
Forgiveness	4.6	1.5	1	6
Empathy	4.4	1.6	1	6
Compassion	4.3	1.7	1	6
Kindness	4.1	1.8	1	6
Generosity	4.0	1.9	1	6
Patience	3.9	2.0	1	6
Self-control	3.7	2.1	1	6
Emotional stability	3.6	2.2	1	6
Psychological well-being	3.5	2.3	1	6
Life purpose	3.4	2.4	1	6
Meaning in life	3.3	2.5	1	6
Existential well-being	3.2	2.6	1	6
Transcendental well-being	3.1	2.7	1	6
Overall well-being	3.0	2.8	1	6

Figure 11a
SEQ ID NO:8
Alpha-Lactalbumin Bot Vector

1 GATCAGTCTCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51 AATACTTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101 ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGGACAGCTTCC
201 AGGAGTTGGTAATGGCCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCTGATTCTG
351 AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501 ATTGTTTATAGCTGTTTATAACCAATATATAACCAATATATTTGGTTATATA
551 GCATGAAGCTTTGATGCCAGCAATTTGAAGGAACCATTTAGAAGTAGTATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651 CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGCTCTGCCTGCAATGTGGGTGATCTGGGTTGCATCCCTGG
751 CTTGGGAAGATCCCCTGGAGAAGGAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAATTCATGGACAGAGGAGCCTTGTAAAGTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGT
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGCTCTCCTGC
951 ATTGCGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001 CTGGAGTGGGTAGCCTATTCTCTCCAGGGGATCTTCCCACCCCAGGAA
1051 TTGAACTGGAGTCTCCTGCATTTTCAGGTGGATCTTCCACAGCTGAACTA
1101 CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATCTGTC
1351 ATACACACTTTTCAAGTTCTCCATTTTTGTGAATAGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTC
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCCTGTTACATGGC
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCCACATCTGCAATCTCTAGGGGGAGGGGG
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTCTTTGTTCTCAAGTAACCAGAGACAGTGTCTC
1751 CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801 GCAGGATCATGTTTGAAGCTCTTCTGGCCAGAGAACAATACCTGCTATG
1851 GACTAGATAGCTGGGAGAGGGGAAAGGAAAGTAGGTTGAATTGAAGGA
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCGACTCTCTCTCATT
1951 CTCTTCTAGATGTAGGCTTGGTACCAGAGCCCCTGAGGCTTCTGTCAT
2001 GAATATAAATATATGAAACTGAGTGATGCTTCCATTTTCAGGTTCTTGGGG
2051 GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101 ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151 CAACACCGCCTCGACCAAGGTTGAGATATCGCGCCGGGACGCGCGGTGGT
2201 AATTACAAGCAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251 GACAATCGCGAACATCTACACACACAACACCGCCTCGACCAGGGTGAGA
2301 TATCGGCCGGGGACGCGCGGTGGTAATTACAAGCGAGATCTCGAGAAGC
2351 TTGTTGGGAATTCAGGCCATCGATCCCGCCGCCACCATTGGAATGGAGCTG
2401 GGTCTTTCTCTTCTTCTCTGTCAGTAACACTACAGGTGCTCACTCCGACATCC
2451 AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
2501 ACTATACATGTCGAGCAAGTGCGGAATATTCACAATTATTTAGCATGGTA
2551 TCAGCAGAAACAGGGAATCTCCTCAGCTCCTGGTCTATAATGCAAAAA
2601 CCTTAGCAGATGGTGTGCCATCAAGGTTTCAGTGGCAGTGGATCAGGAACA
2651 CAATATTCTCTCAAGATCAACAGCCTGCAGCTGGAAGATTTTGGGAGTTA
2701 TTACTGTTCAACATTTTTTGGAGTACTCCGTGGACGTTTCGGTGGAGGCCACA
2751 AGCTGGAATCAACACGGGCTATGCTGCAACCACTGATCCATCTTCCCA
2801 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT

Figure 11b

2851 GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
2901 GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAA
2951 GACAGCACCTACAGCATGAGCAGCACCCCTCACATTGACCAAGGACGAGTA
3001 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
3051 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTT
3101 CCCCTGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAA
3151 GCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACC
3201 ATATTGCCGTCTTTTGGCAATGTGAGGGCCCCGAAACCTGGCCCTGTCTT
3251 CTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAG
3301 GTCTGTTGAATGTGCTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGA
3351 CAAACAACGTCCTGTAGCGACCCTTTCAGGGCAGCGGAACCCCCACCTGG
3401 CGACAGGTGCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA
3451 AGGCGGCACAACCCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501 GTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCCA
3551 GAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT
3601 TTACATGTGTTTAGTCGAGGTTAAAAAACGTCCTAGGCCCCCGAACCAC
3651 GGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTCCTTTG
3701 TCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAGGTT
3751 CAGCTTCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAA
3801 GTTGCTCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTTATGCACT
3851 GGGTGAAGCAGAGGCCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGAT
3901 CCTGCGAATGGGAATACTGAATATGACCCGAAGTTCCAGGGCAAGGCCAC
3951 TATAACAGCAGACACATCCTCCAACACAGTCAACCTGCAGCTCAGCAGCC
4001 TGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGTGGAGGGGAAGTG
4051 GGGTTTCCTTACTGGGGCCAAGGACTCTGGTCACTGTCTCTGCAGCCAA
4101 AACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAA
4151 CTAACCTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG
4201 CCAGTGACAGTGACCTGGAACCTCTGGATCCCTGTCCAGCGGTGTGCACAC
4251 CTTCCACGCTGTCTGTCAGTTTGACCTCTACACTCTGAGCAGCTCAGTGA
4301 CTGTCCCTCCAGCACCTGGCCCAGCGAGACCGTCACTGCAACGTTGCC
4351 CACCCGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTG
4401 TACTAGTGGAGGTGGAGGTAGCCACCATCACCATCACCATTAATCTAGAG
4451 TTAAGCGGCCGTCGAGATCTCGACATCGATAATCAACCTCTGGATTACAA
4501 AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGC
4551 TATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT
4601 ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTGTCTGTCTTTA
4651 TGAGGAGTTGTGGCCCGTTGTGAGGCAACGTGGCGTGGTGTGCACTGTGT
4701 TTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTC
4751 CTTTCCGGGACTTTGCTTTCCCCCTCCCTATTGCCACGGCGGAACATCAT
4801 CGCCGCTGCTTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
4851 ACAATTCCGTGGTGTGTGCGGGAAATCATCGTCCTTTCTTGGCTGCTC
4901 GCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCTTCTGCTACGTCCC
4951 TTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCTGCTGCCGGCTC
5001 TGCGGCTCTTCCGCGTCTTCCGCTTCCGCTCAGACGAGTCGGATCTCC
5051 CTTTGGGCGCCTCCCCGCTGATCGATAAAATAAAAGATTTTATTTAGT
5101 CTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCT
5151 AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
5201 TAGAGAAGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGG
5251 CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGCTCAGGGCCAAG
5301 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
5351 GTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
5401 AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
5451 GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
5501 CTCGCTTCTGTTGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
5551 CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCCGGT
5601 ACCCGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTC

106290-062901

Figure 11c

5651 GCTGTTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701 GGTCTTTCATT

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mtated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

106290-9002680

Figure 12a
SEQ ID NO:9
LSNRL Vector

```

1      TTTGAAAGACCCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51     TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101    GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151    GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201    GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251    AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301    TCATCAGATGTTTCCAGGTGCCCAAGGACCTGAAAATGACCCTGTACC
351    TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTC
401    CGCTCTCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCA
451    GTCTTCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAATAAAGCCT
501    CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCTTGGGAGGGTCTC
551    CTCTGAGTGATTGACTACCCACGACGGGGTCTTTTCATTTGGGGGCTCGT
601    CCGGGATTGAGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGG
651    TAAGCTGGCCAGCAACTTATCTGTCTGTCTCGATTGTCTAGTGTCTATG
701    TTTGATGTTATCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751    CTGGCGGACCCGTGGTGGAAGTACGAGTTCTGAACACCCGGCCGCAACC
801    CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTGTGGCCCGACCTGA
851    GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901    AGGAGACGAGAACCTAAAACAGTTCGCCCTCCGTCTGAATTTTGTCTT
951    CGGTTTGAACCGAAGCCGCGCTCTTGTCTGCTGCAGCCAAGCTTGGGC
1001   TGCAGGTCGAGGACTGGGGACCCTGCACCGAACATGGAGAACACAACATC
1051   AGGATTCTAGGACCCCTGCTCGTGTACAGGCGGGGTTTTCTTGTGTA
1101   CAAGAATCCTCACAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTC
1151   AATTTTCTAGGGGGAGCACCCACGTGTCTGGCCAAAATTTCGAGTCCCC
1201   AACCTCCAATCACTCACCAACCTCTTGTCTCCAATTTGTCTGGCTATC
1251   GCTGGATGTGTCTGCGGCGTTTTATCATATTCTCTTCATCCTGCTGCTA
1301   TGCCTCATCTTCTTGTGGTCTTCTGGACTACCAAGGTATGTTGCCCGT
1351   TTGTCTCTACTTCCAGGAACATCAACTACCAGCACGGGACCATGCAAGA
1401   CCTGCACGATTCTGCTCAAGGAACCTCTATGTTTCCCTCTTGTGCTGT
1451   ACAAAACCTTCGGACGGAACCTGCACTTGTATTCCCATCCCATCATCCTG
1501   GGCTTTTCGAAGATTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGC
1551   TCAGTTTACTAGTGCCATTGTTTCAGTGGTTCGTAGGGCTTTCCCCACT
1601   GTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGCCAAGTCTGTA
1651   CAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTCTTTTGTCTTT
1701   GGGTATACATTTAAACCCTAATAAAACCAAACGTGGGGCTACTCCCTTA
1751   ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801   ATTGTACTAAAAATCAAGCAATGTTTTCGAAAACCTGCCTGTAAATAGACC
1851   TATTGATTGGAAGTATGTCAGAGACTTGTGGGTCTTTTGGGCTTTGCTG
1901   CCCCTTTTACACAATGTGGCTATCCTGCCTTAATGCCTTTATATGCATGT
1951   ATACAATCTAAGCAGGCTTTCACCTTCTCGCCAACTTACAAGGCCTTTCT
2001   GTGTAAACAATATCTGAACCTTTACCCCGTTGCCCGCAACGGTCAGGTC
2051   TCTGCCAAGTGTGCTGACGCAACCCCCACTGGATGGGGCTTGGCTATC
2101   GGCCATAGCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCGATCCATACT
2151   GCGGAACCTCCTAGCAGCTTGTGTTGCTCGCAGGCGGTCTGGAGCGAACT
2201   TATCGGCACCGACAACCTCTGTTGTCTCTCTCGGAAATACACCTCCTTTC
2251   CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCCTCAGGATATAGTAGT
2301   TTCGCTTTTGCATAGGGAGGGGAAATGTAGTCTTATGCAATACACTTGT
2351   AGTCTTGCAACATGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAG
2401   AAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTACGATCGTGC
2451   CTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTG
2501   AATTCCGCATTGTCAGAGATAATTGTATTTAAGTGCCTAGCTCGATACAGC
2551   AAACGCCATTTTTGACCATTACCCACATGGTGTGCACCTTCCAAAGCTT
2601   CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651   ACGTAGAAAGCCAGTCCGCAGAAACGGTGTGACCCCGGATGAATGTCAG
2701   CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAGAGAGAAAGCAGG
2751   TAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGG
2801   ACAGCAAGCGAACCAGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGG

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T06290" 90026860

Figure 12b

2851 GAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGATCTGAT
 2901 GGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC
 2951 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA
 3001 GAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG
 3051 CCGCCGTGTTCCGGCTGTCAGCGCAGGGCGCCCGGTTCTTTTTGTCAAG
 3101 ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCT
 3151 ATCGTGGCTGGCCACGACGGCGCTTCCTTGCGCAGCTGTGCTCGACGTTG
 3201 TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG
 3251 GATCTCCTGTCTATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC
 3301 TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG
 3351 ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA CT CGGATGGAAGCC
 3401 GGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
 3451 AGCCGAACTGTTCCGCCAGGCTCAAGCGCGCATGCCCGACGGCGAGGATC
 3501 TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAA
 3551 GGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
 3601 CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG
 3651 GCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT
 3701 TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGG
 3751 ACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG
 3801 AGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCG
 3851 TTTTCCGGGACGCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
 3901 GAGTTCTTCGCCCACCCCAACCCTGGCCCTATTATTGGGTGGACTAACCA
 3951 TGGGGGGAATTGCCGCTGGAATAGGAACAGGGACTACTGCTCTAATGGCC
 4001 ACTCAGCAATTCCAGCAGCTCCAAGCCGAGTACAGGATGATCTCAGGGA
 4051 GGTGAAAAATCAATCTCTAACCTAGAAAAGTCTCTCACTTCCCTGTCTG
 4101 AAGTTGTCTACAGAATCGAAGGGGCTAGACTTGTTATTTCTAAAAGAA
 4151 GGAGGGCTGTGTGCTGCTCTAAAAGAAGAATGTTGCTTCTATGCGGACCA
 4201 CACAGGACTAGTGAGAGACAGCATGGCCAAATTGAGAGAGAGGCTTAATC
 4251 AGAGACAGAAACTGTTTGAGTCAACTCAAGGATGGTTTGAGGGACTGTTT
 4301 AACAGATCCCCTTGTTTACCACCTTGATATCTACCATTATGGGACCCCT
 4351 CATTGTACTCCTAATGATTTTGCTCTTCGGACCCTGCATTCTTAATCGAT
 4401 TAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTGT
 4451 ACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAA
 4501 ATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
 4551 CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
 4601 AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTGAGGAACAGA
 4651 TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
 4701 GCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAAC
 4751 AGGATATCTGTGGTAAGCAGTTCCTGCCCGGCTCAGGGCCAAGAACAGA
 4801 TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA
 4851 TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA
 4901 CTAACCAATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCG
 4951 AGCTCAATAAAAGAGCCCAACAACCCCTCACTCGGGGCGCCAGTCTCCGA
 5001 TTGACTGAGTCGCGCGGGTACCCGTGATCCAATAAACCCCTCTTGCAAGTT
 5051 GCATCCGACTTGTGGTCTCGCTGTTTCCTTGGGAGGCTCTCCTCTGAGTGA
 5101 TTGACTACCCGTGACGCGGGGTCTTTCATT

1 - 589 MoMuSV 5' LTR
 659 - 897 Retroviral packaging region
 1034 - 1714 Hepatitis B surface antigen
 2279 - 2595 RSV promoter
 2951 - 3745 Neomycin phosphotransferase gene
 4537 - 5130 MoMuLV 3' LTR

Figure 13a
SEQ ID NO:10
Alpha-Lactalbumin cc49IL2 Vector

1 GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51 AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101 AATACTGGGAAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAAGCAAGCTTCC
201 AGGAGTTGCTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351 AAGAGTTGTAGGATATAAAAGTTTGAATAACCTTTAGTTTGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCT
501 ATTGGTTATAGCTGTTTATAACCAATATATAACCAATATATTGGTTATATA
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAAGTATATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTTCAAGT
651 CTTGTTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751 CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATTCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCATGCAGGGTCTCCTGC
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001 CTGGAGTGGGTAGCCTATTCTCTCCAGGGGATCTTCCCATCCAGGAA
1051 TTGAAGTGGAGTCTCCTGCATTTCCAGGTGGATTCTTACCAGCTGAAGT
1101 CCAGGTGGATACTACTCCATATTTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTTTCAAGTTCTCCATTTTGTGAAATAGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGCTCATATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCCACATTTCTGCATGTCTCTAGGGGGGAAGGGG
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTCTTTGTTCCCTCAAGTAACCAGAGACAGTGCTTC
1751 CCAGAACCAACCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801 GCAGGATCATGTTTTGAAGTCTTTCTGGCCAGAGAAACAATACCTGCTATG
1851 GACTAGATACTGGGAGAGGGAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCGTTTTCTGTCTTGGCATGACCAGTCTCTCTTCAAT
1951 CTCTTCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTCTGCAT
2001 GAATATAAATATATGAACTGAGTGATGCTTCCATTTCAAGTTCTTGGGG
2051 GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGAAGCTTTAACCATG
2101 GAATGGAGCTGGGTCTTCTCTTCTTCTGTCTCAGTAACTACAGGTGTCCA
2151 CTCCCAGGTTCAAGTTGCAGCAGTCTGACGCTGAGTTGGTGAAACCTGGGG
2201 CTTCAAGTGAAGATTTCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT
2251 GCAATTCAGTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGG
2301 ATATTTTTTCTCCCGGAAATGATGATTTTTAAATACAATGAGAGGTTCAAGG
2351 GCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAG
2401 CTCAACAGCCTGACATCTGAGGATTCTGCAGTGTATTTCTGTACAAGATC
2451 CCTGAATATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG
2501 GAGGCGGAGGCTACGGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGGACATT
2551 GTGATGTCACAGTCTCCATCCTCCCTACCTGTGTGAGTTGGCGAGAAGGT
2601 TACTTTGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTGGTAATCAAA
2651 AGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
2701 CTGATTTACTGGGCATCCGCTAGGGAATCTGGGGTCCCTGATCGCTTAC
2751 AGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTGTGAAGA
2801 CTGAAGACCTGGCAGTTTATTACTGTGAGCAGTATTATAGCTATCCCCTC

0997006-062901

Figure 13b

2851 ACGTTCGGTGCTGGGACCAAGCTGGTGCTGAAACGGGCGCCGAGCCCAA
2901 ATCTCCTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCC
2951 TGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCTC
3001 ATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCA
3051 CGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
3101 ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
3151 GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA
3201 GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA
3251 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
3301 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCT
3351 GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401 GGCAGCCGAGAGAACAACCTACAAGACCACGCCTCCCGTGCTGGACTCCGAC
3451 GGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
3501 GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC
3551 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGAGGCGGATCA
3601 GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAACCT
3651 GGAGCATTTACTGCTGGATTTACAGATGATTTTGAATGGAATTAATAATT
3701 ACAAGAAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCC
3751 AAGAAGGCCACAGAAGTGAACATCTTCAGTGTCTAGAAGAAGAACTCAA
3801 ACCTCTGGAGGAAGTGCTAAATTTAGCTCAAAGCAAAAACCTTCACTTAA
3851 GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACATAAG
3901 GGATCTGAAACAACATTCTATGTGTGAATATGCTGATGAGACAGCAACCAT
3951 TGTAAGATTTCTGAACAGATGGATTACCTTTTGTCAAAGCATCATCTCAA
4001 CACTAAGTTGAAGCTTGTTAACATCGATAAAATAAAAGATTTTATTTAGT
4051 CTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCT
4101 AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
4151 TAGAGAAGTTTCTGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGG
4201 CCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAG
4251 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
4301 GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
4351 AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
4401 GGACCTGAAATGACCTGTGCCTTATTTGAACTAACAATCAGTTCGCTT
4451 CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
4501 CAACCCCTCACTCGGGGCGCCAGTCCCTCCGATTGACTGAGTCGCCCCGGT
4551 ACCCGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTC
4601 GCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTGAGCGGG
4651 GGTCTTTCATT

1 - 2055 Bovine/human alpha-lactalbumin 5' flanking region
2098 - 4011 cc49-IL2 coding region
4068 - 4661 MoMuLV 3' LTR

Figure 14a
SEQ ID NO:11
Alpha-Lactalbumin YP Vector

```

1   GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51  AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101 ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201 AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351 AAGAGTTGTAGGATATAAAAGTTTGAATAACCTTTAGTTTGGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATAACCAGAAGCTAACAGCT
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAAGTATATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651 CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGCTGCTGCAATGTGGGTGATCTGGGTTTCGATCCCTGG
751 CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACCTGAGCAACTAAGCACAGCACAGTACAGT
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001 CTGGAGTGGGTAGCCTATTCCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051 TTGAACTGGAGTCTCCTGCATTTTCAGGTGGATTCTTCACCAGCTGAACTA
1101 CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601 TGACATACACCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTCTTTGTTCCCTCAAGTAACCAGAGACAGTGCTTC
1751 CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801 GCAGGATCATGGTTTGAAGTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851 GACTAGATACTGGGAGAGGGAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951 CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCTGAGGCTTCTGCAT
2001 GAATATAAATATATGAACTGAGTGATGCTTCCATTTTCAGGTTCTTGGGG
2051 GCGCCGAATTTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101 ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151 CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251 GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301 TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGTTAA
2351 CAGATCTAGGCCTCCTAGGTGACGGATCCCCGGGAATTCGGCGCCGCCA
2401 CCATGATGTCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCC
2451 ACCCAGGCCCCAGGTTCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAAGCC
2501 TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
2551 GCTACTATTTTACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGG
2601 ATTGCATGGATTTATCCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651 CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACA
2701 TGCACCTCAACAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCA
2751 AGGGGTGACCATGATCTTGACTACTGGGGCCAAGGCACCACTCTCACAGT
2801 CTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCCTGGAT

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T06290-90025860

Figure 14b

2851 CTGCTGCCCAAACCTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGC
2901 TATTTCCCTGAGCCAGTGACAGTGACCTGGAACCTCTGGATCCCTGTCCAG
2951 CGGTGTGCACACCTTCCCAGCTGTCTCTGCAGTCTGACCTCTACACTCTGA
3001 GCAGCTCAGTGACTGTCCCCCTCCAGCACCTGGCCCCAGCGAGACCGTCAAC
3051 TGCAACGTTGCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101 GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGCGAGATCTCGAC
3151 GGATCCCCGGGAATTGCGCCCTCTCCCTCCCCCCCCCTAACGTTACTGG
3201 CCGAAGCCGCTTGGAAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTT
3251 CCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCT
3301 GTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAAAGGAA
3351 GCAAGGTCTGTTGAATGTGCTGAAGGAAGCAGTTCCCTCTGGAAGCTTCTT
3401 GAAGACAAACAACGCTGTGATGCGACCCCTTTGCAGGCAGCGGAACCCCCCA
3451 CCTGGCGACAGGTGCCCTCTGCGGCCAAAAGCCACGTTGATAAGATACACC
3501 TGCAAAGGCGGCACAACCCCACTGCCACGTTGTGAGTTGGATAGTTGTGG
3551 AAAGAGTCAAATGGCTCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGGAT
3601 GCCCAGAAGGTACCCCATTTGATTTGGGATCTGATCTGGGCGCTCGGTGCAC
3651 ATGCTTTACATGTGTTTGTAGTGGGTTAAAAAATCTTAGGCCCCCCGA
3701 ACCACGGGGACGTGGTTTTTCTTTGAAAAACACGATGATAATATGGCCTC
3751 CTTTGTCTCTCTGCTCTCTGGTAGGCATCTATTCCATGCCACCCAGGCCG
3801 ACATTGTGCTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAG
3851 AAGGTACACCATGACCTGACGTGCCACCTCAAGTGTAAAGTTACATACACTG
3901 GTACCAGCAGAAGTCAGGACCTCCCCCAAAGATGGATTATGACACAT
3951 CCAAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGAGTGGGTCTGGG
4001 ACCTCTCACTCTCTCACTCAGCAGCATGGAGGCTGAAGATGCTGCCAC
4051 TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTGCGGTGCGGGGACCA
4101 AGCTGGAGCTGAAACCGGGCTGATGCTGCACCAACCTGTATCCATCTTCCCA
4151 CCATCCAGTGAACAGTTAACTCTGGAGGTGCCCTCAGTCGTGTGCTTCTT
4201 GAACAACCTTCTACCCCAAAGACATCAATGTCAAGTGAAGATTGATGGCA
4251 GTGAACGACAAAATGGCGTCTCTGAACAGTTGGACTGATCAGGACAGCAAA
4301 GACAGCACCTACAGCATGAGCAGCACCCCTCACGTTGACCAAGGACGAGTA
4351 TGAACGACATAACAGCTATACCTGTGAGGCCACTACAAGACATCAACTT
4401 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGGGGAGATCT
4451 CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG
4501 GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTTGATACGCTGCTTTA
4551 ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTC
4601 CTTGTATAAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG
4651 TCAGGCAACGCTGGCGTGGTGTGCACTGTGTTTGTCTGACGCAACCCCCACT
4701 GGTTTGGGCGATTGCCAACCCCTGCTCAGCTCCTTTCCGGGACTTTCGCTTT
4751 CCCCCCTCCCTATTGCCACCGCGGAACATCATCGCCGCTGCTTGGCCGCT
4801 GCTGGACAGGGGCTCGGCTGTTGGGCACCTGACAATTCCGTGGTGTGTGCG
4851 GGGAAATCATCGTCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT
4901 TCTGCGCGGGACGTCCTCTGCTACGTCCTTCGGCCCTCAATCCAGCGG
4951 ACCTTCTCTCCCGCGGCCTGCTGCGGGCTCTGCGGCCTCTTCCGCGCTT
5001 CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGCGCCCTCCCCGCC
5051 TGATCGATAAAATAAAGATTTTATTTAGTCTCCGAAAAAGGGGGGAAT
5101 GAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTT
5151 GCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
5201 TCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
5251 AAGCAGTTCCTGCCCCGGCTCAGGGCCCAAGACAGATGGAACAGCTGAAT
5301 ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCGGCTCAGGG
5351 CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGA
5401 GAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCTGTG
5451 CCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTGCGCGGCT
5501 TCTGCTCCCCGAGCTCAATAAAGAGGCCACACCCCTCACTCGGGGCGC
5551 CAGTCTCCGATTGACTGAGTCGCGCGGTACCCGCTGTATCCAATAAAC
5601 CTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCT

Figure 14c

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGTCTTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

105290" 90046360

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

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1      GGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51     CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101    TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151    ACGAGCATTCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201    GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251    CAACGTCTGTAGCGACCCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301    AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351    GGCACAACCCCAAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCA
401    AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451    GTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501    ATGTGTTTtagtCGAGGTTAAAAAACGTCTAGGCCCCCGAACCACGGGG
551    ACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCTTGCTCATCCT
601    TACCTGTCTTGTGGCTGTTGCTCTTGCCGGCGCCATGGGATATCTAGATC
651    TCGAGCTCGCGAAAGCTT

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1 - 583	IRES
584 - 628	Modified bovine alpha-S1 casein signal peptide coding region
629 - 668	Multiple cloning site

T:06290" 90026860

Figure 16a

SEQ ID NO: 13

LNBOEDC Vector

1 TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51 TGCAAGGCATGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101 GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151 GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201 GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301 TCATCAGATGTTTCCAGGGTGCCCAAGGACCTGAAAATGACCTGTACC
351 TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTGCGCGCTTC
401 CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
451 GTCTTCCGATAGACTGCGTCGCCCCGGGTACCCGTATTCCCAATAAAGCCT
501 CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCTTGGGAGGGTCTC
551 CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
601 CCGGAGTTTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGG
651 TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
701 TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751 CTGGCGGACCCGTGGTGGAACTGACGAGTCTGAACACCCGGCCGCAACC
801 CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
851 GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTCTGGT
901 AGGAGACGAGAACCTAAACAGTTCGCCCTCCGTCTGAATTTTGTCTTT
951 CGGTTTGGAAACCGAAGCCGCGCTCTGTCTGCTGCAGCGCTGCAGCATC
1001 GTTCTGTGTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTA
1051 GGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAG
1101 ATGTCGAGCGGATCGCTCACAACCAAGTCGGTAGATGTCAAGAAGAGACGT
1151 TGGGTACCTTCTGCTCTGCAGAAATGGCCAACCTTTAACGTCGGATGGCC
1201 GCGAGACGGCACCTTTAACCGAGACCTCATACCCAGGTTAAGATCAAGG
1251 TCTTTTACCTTGCCCCGCTATGGACACCCAGACCAAGTCCCTACATCGTG
1301 ACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGT
1351 ACACCCTAAGCCTCCGCCTCCTCTTCTCCATCCGCCCCGTCTCTCCCCC
1401 TTGAACCTCCTCGTTCGACCCCGCTCGATCCTCCCTTTATCCAGCCCTC
1451 ACTCCTTCTCTAGGCGCCGGAATFCCGATCTGATCAAGAGACAGGATGAG
1501 GATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
1551 GCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGG
1601 CTGCTCTGATGCCGCCGTGTTCCGGCTGTGACGCGAGGGGCGCCCGGTTT
1651 TTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGTGCAGGACGAG
1701 GCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGT
1751 GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAG
1801 TGCCGGGGCAGGATCTCCTGTCTCATCTCACCTTGCTCCTGCCGAGAAAGTA
1851 TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC
1901 CTGCCCATTTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
1951 GGATGGAAGCCGGTCTTGTCTGATCAGGATGATCTGGACGAAGAGCATCAG
2001 GGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCGA
2051 CGGCGAGGATCTCGTCTGACCCATGGCGATGCCTGCTTGCCGAATATCA
2101 TGGTGGAAAATGGCCGCTTTTCTGGATTGATCGACTGTGGCCGGCTGGGT
2151 GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
2201 AGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCG
2251 CCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC
2301 TTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAAC
2351 CTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGG
2401 CTTCCGAATCGTTTTCGGGACGCGGCTGGATGATCCTCCAGCGCGGGG
2451 ATCTCATGCTGGAGTTCTTCCGCCACCCCGGGCTCGATCCCTCGCGAGT
2501 TGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCA
2551 GTGCAAATCCGTGCGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCC
2601 ATGCCCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAG
2651 GCGGATCCGGCCATTAGCCATATTATTTCATTGGTTATATAGCATAAATCA
2701 ATATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTAC
2751 ATTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATT

099706-062901

Figure 16b

2801 GACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCAT
2851 ATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
2901 CCGCCCAACGACCCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCAT
2951 AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTAC
3001 GGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
3051 CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCA
3101 GTACATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAG
3151 TCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGT
3201 GGATAGCGGTTTGA CTACGCGGGATTTC CAAGTCTCCACCCCATTTGACGT
3251 CAATGGGAGTTTGT TTTGGCACCAAAATCAACGGGACTTTCCAAAATGTC
3301 GTAACAACTCCGCCCATTTGACGCAAATGGGCGGTAGGCATGTACGGTGG
3351 GAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG
3401 ACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCA
3451 GCCTCCGCGGCCCAAGCTTCTCGACGGATCCCGGGAATTCAGGCCATC
3501 GATCCCGCGGCCACCATGGAATGGAGCTGGGTCTTTCTCTTCTTCTGTC
3551 AGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601 CCCTATCTGCATCTGTGGGAGAACTGTCACTATCAGATGTGAGCAAGT
3651 GGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATC
3701 TCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCAT
3751 CAAGGTTCA GTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
3801 AGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAG
3851 TACTCCGTGGACGTTCCGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTG
3901 ATGCTGCACCAACTGTATCCATCTTCCACCATCCAGTGAGCAGTTAACA
3951 TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGA
4001 CATCAATGTCAAGTGGAGATTGATGGCAGTGAACGACAAAATGGCGTCC
4051 TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101 AGCACCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAC
4151 CTGTGAGGCCACTCACAAGACATCAACTTCAACCATTTGTCAAGAGCTTCA
4201 ACAGGAATGAGTGTGAAAGCATCGATTTCCCTGAATTGCCCCCTCTCC
4251 CTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAAATAAGGCCGGT
4301 GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAAT
4351 GTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCTAGGGG
4401 TCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGG
4451 AAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACC
4501 CTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCA
4551 AAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAAGTCC
4601 ACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGC
4651 GTATTCAACAAGGGGCTGAAGGATGCCAGAGGTACCCCATTTGTATGGG
4701 ATCTGATCTGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGT
4751 TAAAAAACGCTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCTTTGA
4801 AAAACACGATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCA
4851 TCCTATTCCATGCCACCCAGGCCGAGGTTTCAAGTTCAGCAGTCTGGGGCA
4901 GAGCTTGTGAAGCCAGGGGCTCAGTCAAGTTGTCTGCACAGCTTCTGG
4951 CTTCAACATTAAAGACACCTTTATGCACTGGGTGAAGCAGAGGCCTGAAC
5001 AGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGGAATACTGAA
5051 TATGACCCGAAGTTCAGGGCAAGGCCACTATAACAGCAGACACATCCTC
5101 CAACACAGTCAACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCG
5151 TCTATTACTGTGCTAGTGGAGGGGAACTGGGGTTTCTTACTGGGGCCAA
5201 GGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACACCCCATCTGTCTA
5251 TCCACTGGCCCTGGATCTGCTGCCCAAATAACTCCATGGTGACCTGG
5301 GATGCCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAAC
5351 TCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTGACAGTC
5401 TGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGC
5451 CCAGCGAGACCGTCACCTGCAACGTTGCCACCCGGCCAGCAGCACCAAG
5501 GTGGACAAGAAAATTTGTCAGGGGATTGTACTAGTGGAGGTGGAGGTAG
5551 CCACCATCACCATCAACATTAATCTAGAGTTAAGCGGCCGTCGAGATCTA
5601 GGCTCCTAGGTGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAG
5651 AAAAAGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTA
5701 AGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGAGAATAGAGA
5751 AGTTCAGATCAAGGTGAGGAACAGATGGAACAGCTGAATATGGGGCAAAC
5801 AGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGA
5851 TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT

0987006-062904

Figure 16c

5901 GCCCCGGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
5951 CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT
6001 GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCT
6051 TCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101 CTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCCGGGTACCCGT
6151 GTATCCAATAAACCCCTCTTGAGTTGCATCCGACTTGTGGTCTCGCTGTT
6201 CCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTT
TCATT

Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α -LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

105290-9002550

Figure 17a
SEQ ID NO: 34
LNBOTDC Vector

1 GAATTAATTCATACCAGATCACCGAAAACGTCTCCAAATGTGTCCCCC
51 TCACACTCCCAAATTCGCGGGCTTCTGCCTCTTAGACCACTCTACCCTAT
101 TCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTT
151 TGAAAGACCCCAACCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
201 CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTTCAAGTCAAGGT
251 CAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGG
301 TTCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGG
351 CCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCTCGGGGCCAAG
401 AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATC
451 ATCAGATGTTTCCAGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTT
501 ATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCCG
551 CTCTCCGAGCTCAATAAAAGAGCCACAACCCCTCACTCGGCGCGCCAGT
601 CTTCCGATAGACTGCGTTCGCGGGGTACCCGTATTCCCAATAAAGCCTCT
651 TGCTGTTTGCATCCGAATCGTGCTCGCTGTTCTTGGGAGGGTCTCCT
701 CTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCC
751 GGGATTTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGGTA
801 AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTT
851 TGATGTTATGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCT
901 GCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGCGCAACCCCT
951 GGGAGACGTCCAGGGACTTTGGGGGCGGTTTTTGTGGCCCGACCTGAGG
1001 AAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAG
1051 GAGACGAGAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTGTCTTTCG
1101 GTTTGGAACCGAAGCCGCGCGTCTGTGTCTGCTGCAGCGCTGCAGCATCGT
1151 TCTGTGTTGTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG
1201 GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCAGTGGAAGAT
1251 GTCGAGCGGATCGCTCACAAACAGTCGGTAGATGTCAAGAAGAGACGTTG
1301 GGTACCTTCTGCTCTGCAGAAATGGCCAACCTTTAACGTCGGATGGCCGC
1351 GAGACGGCACCTTTAACCGAGACCTCATCAACAGGTTAAGATCAAGGTC
1401 TTTTCACCTGGCCCGCATGGACACCCAGACAGGTCCCCTACATCGTGAC
1451 CTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTAC
1501 ACCCTAAGCCTCCGCTCCTCTTCTCCATCCGCCCCGTCTCTCCCCCTT
1551 GAACCTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
1601 TCCTTCTCTAGGCGCCGGAATTCGATCTGATCAAGAGACAGGATGAGGG
1651 AGCTTGATATATCAATTTTCGGATCTGATCAGCACGTGTTGACAATTAATC
1701 ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAA
1751 CCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCA
1801 ACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG
1851 CGCAGCTCTCTCTAGCGACGGCCGATCTTCACTGGTGTCAATGTATATC
1901 ATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGTGGGCACTGCTGCT
1951 GCTGCGGCAGCTGGCAACCTGACTTGATCGTCGCGATCGGAAATGAGAA
2001 CAGGGGCATCTTGAGCCCTGCGGACGGTGTGACAGGTGCTTCTCGATC
2051 TGCATCCTGGGATCAAAGCGATAGTGAAGGACAGTGATGGACAGCCGACG
2101 GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA
2151 AGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTTCGAT
2201 TCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA
2251 CGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCG
2301 CCCACCCCAACTTGTTTATTCAGCTTATAATGGTTACAAATAAAGCAAT
2351 AGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
2401 TGGTTTGTCCAACTCATCAATGTATCTTATCATGTCTGTACGAGTTGGT
2451 TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501 AAATCCGTCGGCATCCAGGAAACAGCAGCGGCTATCCGCGCATCCATGC
2551 CCCCAGACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTTCGAGGCGG
2601 ATCCGGCCATTAGCCATATTTATTCATTGGTTATATAGCATAAATCAATAT
2651 TGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTT
2701 ATATTGGCTCATGTCACATTACCGCCATGTTGACATTGATTATTGACT
2751 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATAT
2801 GGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGC
2851 CCAACGACCCCCGCCATTGACCTCAATAATGACGTATGTTCCCATAGTA

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Figure 17b

2901 ACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA
 2951 AACTGCCCACCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC
 3001 CTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAGTAC
 3051 ATGACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCAT
 3101 CGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGAT
 3151 AGCGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATTGACGTCAAT
 3201 GGGAGTTTGTTTTGGCACC AAAATCAACGGGACTTTCCAAAATGTGTA
 3251 CAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCATGTACGGTGGGAGG
 3301 TCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGC
 3351 CATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCT
 3401 CCGCGGCCCCCAAGCTTCTCGAGTTAACAGATCTAGGCTGGCAGACAGGT
 3451 TTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAG
 3501 CTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTAT
 3551 GTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
 3601 ACCATGATTACGCCAAGCTTGGCTGCAGGTCGACGGATCCACTAGTAACG
 3651 GCGGCCAGTGTGCTGGAATTCACCATGGGGCAACCGGGAACGGCAGCGC
 3701 CTTCTTGCTGGCACC CAATGGAAGCCATGCGCCGGACACGACGTACGCG
 3751 AGCAAAGGGACGAGGTGTGGGTGGTGGGCATGGGCATCGTCATGTCTCTC
 3801 ATCGTCTTGCCCATCGTGTTTGGCAATGTGCTGGTCATCACAGCCATTGC
 3851 CAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACAGCTTGG
 3901 CCTGTGCTGATCTGGTCATGGGGCTAGCAGTGGTGGCCTTTGGGGCCGCC
 3951 CATATTCTCATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTCTG
 4001 GACTTCCATTGATGTGCTGTGCGTCACGGCATCGATTGAGACCCTGTGCG
 4051 TGATCGCAGTCGACCGCTACTTTGCCATTACTAGTCCTTTCAAGTACCAG
 4101 AGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGAT
 4151 TGTGTCAGGCCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACAGGG
 4201 CCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGAC
 4251 TTCTTCACGAACCAAGCCTATGCCATTGCCCTCTTCCATCGTGTCTTCTA
 4301 CGTTCCCCCTGGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGG
 4351 CCAAAAGGCAGCTCCAGAAGATTGACAAAATCTGAGGGCCGCTTCCATGTC
 4401 CAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGGCATGGACTCCG
 4451 CAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAG
 4501 GCATCATCATGGGCACCTTTCACCCCTCTGCTGGCTGCCCTTCTTCATCGTT
 4551 AACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACAT
 4601 CCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCTTATCT
 4651 ACTGCCGGAGCCCAGATTTTCAAGGATTGCCTTCCAGGAGCTTCTGTGCTG
 4701 CGCAGGTCTTCTTTGAAGGCCTATGGCAATGGCTACTCCAGCAACGGCAA
 4751 CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAATAAAC
 4801 TGCTGTGTGAAGACCTCCAGGCACGGAAGACTTTGTGGGCCATCAAGGT
 4851 ACTGTGCCTAGCGATAACATTGATTACAAAGGGAGGAATTGTAGTACAAA
 4901 TGACTCACTGCTCTCGAGAAATCGAGGGGCGGCACCACCATCATCACCACG
 4951 TCGACCCCGGGGACTACAAGGATGACGATGACAAGTAAGCTTTATCCATC
 5001 AACTTGGCGGCCGCTCGAGCATGCATCTAGCGGCCGCTCGAGGCCGGCAA
 5051 GGCCGGATCCCCGGGAATTGCCCCCTCTCCCTCCCCCCCCCTAACGTTA
 5101 CTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
 5151 TTTTCCACCATATTGCCGCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
 5201 CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCTCTCTGCCAAAG
 5251 GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCT
 5301 TCTTGAAGACAAACAACGTCCTGTAGCGACCCCTTTGCAGGCAGCGGAACCC
 5351 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
 5401 CACCTGCAAAGGCGGCACAACCCCAAGTCCACGTTGTGAGTTGGATAGTT
 5451 GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
 5501 GGATGCCCAGAAGGTACCCCATTTGATGGGATCTGATCTGGGGCCTCGGT
 5551 GCACATGCTTTACATGTGTTAGTCGAGGTTAAAAAACGTTAGGCCCCC
 5601 CCGAACCAAGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGG
 5651 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTTCCATGCCACCCAG
 5701 GCGGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAG
 5751 GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTGTTGTACAGCTCCAACA
 5801 ATAAGAACTATTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCTAAG
 5851 CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT
 5901 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
 5951 AGGCTGAAGATGTGGCAGTTTATTACTGTGAGCAATATTATAGTACTCAG

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Figure 17c

6001 ACGTTCGGCCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACC
6051 ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGT
6101 CCTCTGTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
6151 CAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT
6201 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGA
6251 CGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTC
6301 ACCCATCAGGGCCTGAGATCGCCCGTCAAAAGAGCTTCAACAAGGGGAG
6351 AGTGTAGTTCTAGATAATTAATTAGGAGGAGATCTCGAGCTCGCGAAAG
6401 CTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCCTGGCG
6451 TTACCCAACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGCCTCCTA
6501 GGTGCACATCGATAAAATAAAAGATTTTTATTTAGTCTCCAGAAAAAGGGG
6551 GGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC
6601 ATTTTGCAAGGCATGGAATAATACATAACTGAGAATAGAGAAGTTCAGAT
6651 CAAGGTGAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCT
6701 GTGGTAAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGC
6751 TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCCGGCT
6801 CAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTT
6851 CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACC
6901 CTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTGCG
6951 GCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCACAAACCCCTCACTCGG
7001 GGCGCCAGTCTCCCGATTGACTGAGTCGCGCGGTACCCGTGTATCCAAT
7051 AAACCCCTCTTGACGTTGCATCCGACTTGTGGTCTCGCTGTTCCCTGGGAG
7101 GGTCTCCTCTGAGTGATTGACTACCCGTGACGCGGGGTCTTTCATTTGGG
7151 GGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACACCGACCCACCAC
7201 CGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACC
7251 TCTGACACATGCAGTCCCCGAGACGGTCACAGCTTGTCTGTAAGCGGAT
7301 GCCGGGATAACGCAGGAAAGAACATGTGAGCAAAGGCCAGCAAAGGCC
7351 TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401 GCTTAATATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGC
7451 GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC
7501 TCTTCCGCTTCTCTCGCTCACTGACTCGCTGCGCTCGGTGTTCCGGCTGCG
7551 GCGAGCGGTATCAGTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT
7601 CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAGGCCAGCAAAGGCC
7651 AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC
7701 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
7751 CGACAGGACTATAAAGATACCGGCGTTTCCCCCTGGAAGCTCCCTCGTG
7801 CGCTCTCCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCCGCCTTCT
7851 CCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCA
7901 GTTCGGTGTAGTTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC
7951 GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAA
8001 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
8051 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG
8101 CCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
8151 GAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
8201 AAACCAACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACG
8251 CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
8301 TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT
8351 TATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAAAAATGAAGTTTT
8401 AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451 CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCA
8501 TAGTTGCCTGACTCCCCGTGCTGTAGATAACTACGATACGGGAGGGCTTA
8551 CCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGC
8601 TCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAA
8651 GTGGTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGG
8701 GAAGCTAGAGTAAGTAGTTCCGCAGTTAATAGTTTGGCAACGTTGTTGC
8751 CATTGCTGACGAGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCAT
8801 TCAGTCCCGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG
8851 TGCAAAAAAGCGGTTAGTCTCTCGGTCTCCGATCGTTGTGAGAAGTAA
8901 GTTGGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTC
8951 TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCA
9001 ACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC
9051 GCGGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGTGC

Figure 17d

9101 TCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCG
9151 CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
9201 AGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGC
9251 AAAATGCCGCAAAAAGGGAATAAGGGCGACACGAAATGTTGAATACTC
9301 ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT
9351 CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG
9401 TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451 ATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCG
1. TCTTCAAGAAT

Features:

149-737 Moloney murine sarcoma virus 5' LTR
807-1616 Extended Packaging Region
1680-1735 EM7 promoter (bacteriophage T7 promoter)
1754-2151 Blasticidin resistance gene coding sequence
2310-2440 SV40 poly A signal and site
2603-3420 CMV IE promoter
3675-4988 G-protein-coupled receptor (GPCR)
5071-5646 IRES
5647-5703 Bovine a-lactalbumin signal peptide
5704-6372 'humanized' antibody light chain
6553-7146 MoMuLV 3' LTR
7683Origin of replication
9302-8442 b-Lactmase coding sequence

FO6250-90065550